
Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=8; day=21; hr=15; min=0; sec=34; ms=475;]

Validated By CRFValidator v 1.0.3

Application No: 10565126 Version No: 2.0

Input Set:

Output Set:

Started: 2009-08-07 09:52:59.981 **Finished:** 2009-08-07 09:53:16.737

Elapsed: 0 hr(s) 0 min(s) 16 sec(s) 756 ms

Total Warnings: 13
Total Errors: 0

No. of SeqIDs Defined: 146

Actual SeqID Count: 146

Error code		Error Description										
W	402	Undefined organism found in <213> in SEQ ID (2)										
W	402	Undefined organism found in <213> in SEQ ID (3)										
W	402	Undefined organism found in <213> in SEQ ID (18)										
W	213	Artificial or Unknown found in <213> in SEQ ID (137)										
W	213	Artificial or Unknown found in <213> in SEQ ID (138)										
W	213	Artificial or Unknown found in <213> in SEQ ID (139)										
W	213	Artificial or Unknown found in <213> in SEQ ID (140)										
W	213	Artificial or Unknown found in <213> in SEQ ID (141)										
W	213	Artificial or Unknown found in <213> in SEQ ID (142)										
W	213	Artificial or Unknown found in <213> in SEQ ID (143)										
W	213	Artificial or Unknown found in <213> in SEQ ID (144)										
W	213	Artificial or Unknown found in <213> in SEQ ID (145)										
W	213	Artificial or Unknown found in <213> in SEQ ID (146)										

SEQUENCE LISTING

<110> Grandi, Guido Telford, John Bensi, Giuliano

<120> IMMUNOGENIC COMPOSITIONS FOR STREPTOCOCCUS PYOGENES

<130> PP020663.0004

<140> 10565126

<141> 2006-09-18

<150> PCT/US04/24868

<151> 2004-07-30

<150> US 60/491,822

<151> 2003-07-31

<150> US 60/541,565

<151> 2004-02-03

<160> 146

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 873

<212> PRT

<213> Streptococcus pyogenes

<400> 1

Met Asp Leu Glu Gln Thr Lys Pro Asn Gln Val Lys Gln Lys Ile Ala
1 5 10 15

Leu Thr Ser Thr Ile Ala Leu Leu Ser Ala Ser Val Gly Val Ser His 20 25 30

Gln Val Lys Ala Asp Asp Arg Ala Ser Gly Glu Thr Lys Ala Ser Asn 35 40 45

Thr His Asp Asp Ser Leu Pro Lys Pro Glu Thr Ile Gln Glu Ala Lys
50 60

Ala Thr Ile Asp Ala Val Glu Lys Thr Leu Ser Gln Gln Lys Ala Glu 65 70 75 80

Leu Thr Glu Leu Ala Thr Ala Leu Thr Lys Thr Thr Ala Glu Ile Asn 85 90 95

His Leu Lys Glu Gln Gln Asp Asn Glu Gln Lys Ala Leu Thr Ser Ala 100 105 110

Gln Glu Ile Tyr Thr Asn Thr Leu Ala Ser Ser Glu Glu Thr Leu Leu 115 120 125

Ala Gln Gly Ala Glu His Gln Arg Glu Leu Thr Ala Thr Glu Thr Glu
130 135 140

Glu Gln Lys Ala Ser Ile Ser Ala Glu Thr Thr Arg Ala Gln Asp Leu 165 170 175

Val Glu Gln Val Lys Thr Ser Glu Gln Asn Ile Ala Lys Leu Asn Ala

180 185 190

Met	Ile	Ser 195	Asn	Pro	Asp	Ala	Ile 200	Thr	Lys	Ala	Ala	Gln 205	Thr	Ala	Asn
Asp	Asn 210	Thr	Lys	Ala	Leu	Ser 215	Ser	Glu	Leu	Glu	Lys 220	Ala	Lys	Ala	Asp
Leu 225	Glu	Asn	Gln	Lys	Ala 230	Lys	Val	Lys	Lys	Gln 235	Leu	Thr	Glu	Glu	Leu 240
	Ala	Gln	Lys	Ala 245		Leu	Ala	Glu	Lys 250		Ala	Glu	Leu	Ser 255	
Leu	Lys	Ser	Ser 260		Pro	Ser	Thr	Gln 265		Ser	Ile	Val	Gly 270		Asn
Thr	Met	Lys 275	Ala	Pro	Gln	Gly	Tyr 280	Pro	Leu	Glu	Glu	Leu 285	Lys	Lys	Leu
Glu	Ala 290	Ser	Gly	Tyr	Ile	Gly 295	Ser	Ala	Ser	Tyr	Asn 300	Asn	Tyr	Tyr	Lys
Glu 305	His	Ala	Asp	Gln	Ile 310		Ala	Lys	Ala	Ser 315	Pro	Gly	Asn	Gln	Leu 320
	Gln	Tyr	Gln	Asp 325	Ile	Pro	Ala	Asp	Arg	Asn	Arg	Phe	Val	Asp 335	
Asp	Asn	Leu	Thr	Pro	Glu	Val	Gln	Asn 345	Glu	Leu	Ala	Gln	Phe 350	Ala	Ala
His	Met	Ile 355	Asn	Ser	Val	Arg	Arg 360	Gln	Leu	Gly	Leu	Pro 365	Pro	Val	Thr
Val	Thr 370	Ala	Gly	Ser	Gln	Glu 375	Phe	Ala	Arg	Leu	Leu 380	Ser	Thr	Ser	Tyr
Lys 385	Lys	Thr	His	Gly	Asn 390	Thr	Arg	Pro	Ser	Phe 395	Val	Tyr	Gly	Gln	Pro 400
Gly	Val	Ser	Gly	His	Tyr	Gly	Val	Gly	Pro 410	His	Asp	Lys	Thr	Ile 415	Ile
Glu	Asp	Ser	Ala 420	Gly	Ala	Ser	Gly	Leu 425	Ile	Arg	Asn	Asp	Asp	Asn	Met
Tyr	Glu	Asn 435	Ile	Gly	Ala	Phe	Asn 440	Asp	Val	His	Thr	Val	Asn	Gly	Ile
Lys	Arg 450	Gly	Ile	Tyr	Asp	Ser 455	Ile	Lys	Tyr	Met	Leu 460	Phe	Thr	Asp	His
Leu 465	His	Gly	Asn	Thr	Tyr 470	Gly	His	Ala	Ile	Asn 475	Phe	Leu	Arg	Val	Asp 480
Lys	His	Asn	Pro	Asn 485	Ala	Pro	Val	Tyr	Leu 490	Gly	Phe	Ser	Thr	Ser 495	Asn
Val	Gly	Ser	Leu 500	Asn	Glu	His	Phe	Val 505	Met	Phe	Pro	Glu	Ser 510	Asn	Ile
Ala	Asn	His 515	Gln	Arg	Phe	Asn	Lys 520	Thr	Pro	Ile	Lys	Ala 525	Val	Gly	Ser
Thr	Lys 530	Asp	Tyr	Ala	Gln	Arg 535	Val	Gly	Thr	Val	Ser 540	Asp	Thr	Ile	Ala
Ala 545	Ile	Lys	Gly	Lys	Val 550	Ser	Ser	Leu	Glu	Asn 555	Arg	Leu	Ser	Ala	Ile 560
His	Gln	Glu	Ala	Asp 565	Ile	Met	Ala	Ala	Gln 570	Ala	Lys	Val	Ser	Gln 575	Leu
Gln	Gly	Lys	Leu 580	Ala	Ser	Thr	Leu	Lys 585	Gln	Ser	Asp	Ser	Leu 590	Asn	Leu
Gln	Val	Arg 595	Gln	Leu	Asn	Asp	Thr 600	Làs	Gly	Ser	Leu	Arg 605	Thr	Glu	Leu
Leu	Ala 610	Ala	Lys	Ala	Lys	Gln 615	Ala	Gln	Leu	Glu	Ala 620	Thr	Arg	Asp	Gln
Ser	Leu	Ala	Lys	Leu	Ala	Ser	Leu	Lys	Ala	Ala	Leu	His	Gln	Thr	Glu
625					630					635					640
Ala	Leu	Ala	Glu	Gln	Ala	Ala	Ala	Arg	Val	Thr	Ala	Leu	Val	Ala	Lys

645 650 Lys Ala His Leu Gln Tyr Leu Arg Asp Phe Lys Leu Asn Pro Asn Arg 665 Leu Gln Val Ile Arg Glu Arg Ile Asp Asn Thr Lys Gln Asp Leu Ala 680 Lys Thr Thr Ser Ser Leu Leu Asn Ala Gln Glu Ala Leu Ala Ala Leu 695 700 Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr Ile Ala Thr Thr Glu His 710 715 Gln Leu Thr Leu Lys Thr Leu Ala Asn Glu Lys Glu Tyr Arg His 725 730 Leu Asp Glu Asp Ile Ala Thr Val Pro Asp Leu Gln Val Ala Pro Pro 740 745 Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser Lys Ile Asp Thr Thr Pro 760 Leu Val Gln Glu Met Val Lys Glu Thr Lys Gln Leu Leu Glu Ala Ser 770 775 780 Ala Arg Leu Ala Ala Glu Asn Thr Ser Leu Val Ala Glu Ala Leu Val 790 795 Gly Gln Thr Ser Glu Met Val Ala Ser Asn Ala Ile Val Ser Lys Ile 805 810 Thr Ser Ser Ile Thr Gln Pro Ser Ser Lys Thr Ser Tyr Gly Ser Gly 820 825 Ser Ser Thr Thr Ser Asn Leu Ile Ser Asp Val Asp Glu Ser Thr Gln 840 Arg Ala Leu Lys Ala Gly Val Val Met Leu Ala Ala Val Gly Leu Thr 855 860 Gly Phe Arg Phe Arg Lys Glu Ser Lys 865 870

<210> 2

<211> 2622

<212> DNA

<213> S. pyogenes

<400> 2

atggacttag aacaaacgaa gccaaaccaa gttaagcaga aaattgcttt aacctcaaca 60 120 attgetttat tgagtgecag tgtaggegta teteaceaag teaaageaga tgatagagee tcaggagaaa cgaaggcgag taatactcac gacgatagtt taccaaaacc agaaacaatt 180 caagaggcaa aggcaactat tgatgcagtt gaaaaaactc tcagtcaaca aaaagcagaa 240 300 ctgacagagc ttgctaccgc tctgacaaaa actactgctg aaatcaacca cttaaaagag cagcaagata atgaacaaaa agctttaacc tctgcacaag aaatttacac taatactctt 360 420 gcaagtagtg aggagacgct attagcccaa ggagccgaac atcaaagaga gttaacagct 480 actgaaacag agcttcataa tgctcaagca gatcaacatt caaaagagac tgcattgtca gaacaaaaag ctagcatttc agcagaaact actcgagctc aagatttagt ggaacaagtc 540 600 aaaacgtctg aacaaaatat tgctaagctc aatgctatga ttagcaatcc tgatgctatc actaaagcag ctcaaacggc taatgataat acaaaagcat taagctcaga attggagaag 660 gctaaagctg acttagaaaa tcaaaaagct aaagttaaaa agcaattgac tgaagagttg 720 780 gcagctcaga aagctgctct agcagaaaaa gaggcagaac ttagtcgtct taaatcctca 840 gctccgtcta ctcaagatag cattgtgggt aataatacca tgaaagcacc gcaaggctat cctcttgaag aacttaaaaa attagaagct agtggttata ttggatcagc tagttacaat 900 aattattaca aagagcatgc agatcaaatt attgccaaag ctagtccagg taatcaatta 960 aatcaatacc aagatattcc agcagatcgt aatcgctttg ttgatcccga taatttgaca 1020 ccagaagtgc aaaatgagct agcgcagttt gcagctcaca tgattaatag tgtaagaaga 1080 caattaggtc taccaccagt tactgttaca gcaggatcac aagaatttgc aagattactt 1140 agtaccaget ataagaaaac teatggtaat acaagaceat eatttgteta eggacageea 1200 ggggtatcag ggcattatgg tgttgggcct catgataaaa ctattattga agactctgcc 1260

```
ggagcgtcag ggctcattcg aaatgatgat aacatgtacg agaatatcgg tgcttttaac
                                                                      1320
gatgtgcata ctgtgaatgg tattaaacgt ggtatttatg acagtatcaa gtatatgctc
                                                                     1380
tttacagatc atttacacgg aaatacatac ggccatgcta ttaacttttt acgtgtagat
                                                                      1440
aaacataacc ctaatqcqcc tqtttacctt qqattttcaa ccaqcaatqt aqqatctttq
                                                                     1500
aatgaacact ttgtaatgtt tccagagtct aacattgcta accatcaacg ctttaataag
                                                                      1560
acccctataa aagccgttgg aagtacaaaa gattatgccc aaagagtagg cactgtatct
                                                                     1620
gatactattg cagcgatcaa aggaaaagta agctcattag aaaatcgttt gtcggctatt
                                                                     1680
catcaagaag ctgatattat ggcagcccaa gctaaagtaa gtcaacttca aggtaaatta
                                                                      1740
qcaaqcacac ttaaqcaqtc aqacaqctta aatctccaaq tqaqacaatt aaatqatact
                                                                     1800
aaaggttett tgagaacaga attactagca getaaagcaa aacaagcaca actegaaget
                                                                      1860
actcgtgatc aatcattagc taagctagca tcgttgaaag ccgcactgca ccagacagaa
                                                                     1920
gccttagcag agcaagccgc agccagagtg acagcactgg tggctaaaaa agctcatttg
                                                                     1980
caatatctaa gggactttaa attgaatcct aaccgccttc aagtgatacg tgagcgcatt
                                                                      2040
gataatacta agcaagattt ggctaaaact acctcatctt tgttaaatgc acaagaagct
                                                                     2100
ttaqcaqcct tacaaqctaa acaaaqcaqt ctaqaaqcta ctattqctac cacaqaacac
                                                                      2160
                                                                     2220
cagttgactt tgcttaaaac cttagctaac gaaaaggaat atcgccactt agacgaagat
atagctactg tgcctgattt gcaagtagct ccacctctta cgggcgtaaa accgctatca
                                                                     2280
tatagtaaga tagatactac tccgcttgtt caagaaatgg ttaaagaaac gaaacaacta
                                                                     2340
ttagaagett cagcaagatt agetgetgaa aatacaagte ttgtagcaga agegettgtt
                                                                     2400
ggccaaacct ctgaaatggt agcaagtaat gccattgtgt ctaaaatcac atcttcgatt
                                                                      2460
actcagccct catctaagac atcttatggc tcaggatctt ctacaacgag caatctcatt
                                                                     2520
tctgatgttg atgaaagtac tcaaagagct cttaaagcag gagtcgtcat gttggcagct
                                                                     2580
gtcggcctca caggatttag gttccgtaag gaatctaagt ga
                                                                      2622
<210> 3
<211> 26
<212> PRT
<213> S. pyogenes
<400> 3
Met Asp Leu Glu Gln Thr Lys Pro Asn Gln Val Lys Gln Lys Ile Ala
                 5
                                    1.0
                                                        1.5
Leu Thr Ser Thr Ile Ala Leu Leu Ser Ala
            20
                                2.5
<210> 4
<211> 78
<212> DNA
<213> Streptococcus pyogenes
<400> 4
      atggacttag aacaaacgaa gccaaaccaa gttaagcaga aaattgcttt aacctcaaca
                                                                              60
      attgctttat tgagtgcc
                                                                              78
<210> 5
<211> 847
<212> PRT
<213> Streptococcus pyogenes
<400> 5
      Ser Val Gly Val Ser His Gln Val Lys Ala Asp Asp Arg Ala Ser Gly
                       5
                                          10
      Glu Thr Lys Ala Ser Asn Thr His Asp Asp Ser Leu Pro Lys Pro Glu
                                      25
```

Thr Ile Gln Glu Ala Lys Ala Thr Ile Asp Ala Val Glu Lys Thr Leu

45

40

35

Ser	Gln 50	Gln	Lys	Ala	Glu	Leu 55	Thr	Glu	Leu	Ala	Thr 60	Ala	Leu	Thr	Lys
Thr 65	Thr	Ala	Glu	Ile	Asn 70	His	Leu	Lys	Glu	Gln 75	Gln	Asp	Asn	Glu	Gln 80
Lys	Ala	Leu	Thr	Ser 85	Ala	Gln	Glu	Ile	Tyr 90	Thr	Asn	Thr	Leu	Ala 95	Ser
Ser	Glu	Glu	Thr 100	Leu	Leu	Ala	Gln	Gly 105	Ala	Glu	His	Gln	Arg 110	Glu	Leu
Thr	Ala	Thr 115	Glu	Thr	Glu	Leu	His 120	Asn	Ala	Gln	Ala	Asp 125	Gln	His	Ser
Lys	Glu 130	Thr	Ala	Leu	Ser	Glu 135	Gln	Lys	Ala	Ser	Ile 140	Ser	Ala	Glu	Thr
Thr 145	Arg	Ala	Gln	Asp	Leu 150	Val	Glu	Gln	Val	Lys 155	Thr	Ser	Glu	Gln	Asn 160
Ile	Ala	Lys	Leu	Asn 165	Ala	Met	Ile	Ser	Asn 170	Pro	Asp	Ala	Ile	Thr 175	Lys
Ala	Ala	Gln	Thr 180	Ala	Asn	Asp	Asn	Thr 185	Lys	Ala	Leu	Ser	Ser 190	Glu	Leu
Glu	Lys	Ala 195	Lys	Ala	Asp	Leu	Glu 200	Asn	Gln	Lys	Ala	Lys 205	Val	Lys	Lys
Gln	Leu 210	Thr	Glu	Glu	Leu	Ala 215	Ala	Gln	Lys	Ala	Ala 220	Leu	Ala	Glu	Lys
Glu 225	Ala	Glu	Leu	Ser	Arg 230	Leu	Lys	Ser	Ser	Ala 235	Pro	Ser	Thr	Gln	Asp 240
Ser	Ile	Val	Gly	Asn 245	Asn	Thr	Met	Lys	Ala 250	Pro	Gln	Gly	Tyr	Pro 255	Leu
Glu	Glu	Leu	Lys 260	Lys	Leu	Glu	Ala	Ser 265	Gly	Tyr	Ile	Gly	Ser 270	Ala	Ser
Tyr	Asn	Asn 275	Tyr	Tyr	Lys	Glu	His 280	Ala	Asp	Gln	Ile	Ile 285	Ala	Lys	Ala
Ser	Pro 290	Gly	Asn	Gln	Leu	Asn 295	Gln	Tyr	Gln	Asp	Ile 300	Pro	Ala	Asp	Arg
Asn 305	Arg	Phe	Val	Asp	Pro 310	Asp	Asn	Leu	Thr	Pro 315	Glu	Val	Gln	Asn	Glu 320
Leu	Ala	Gln	Phe	Ala 325	Ala	His	Met	Ile	Asn 330	Ser	Val	Arg	Arg	Gln 335	Leu
Gly	Leu	Pro	Pro 340	Val	Thr	Val	Thr	Ala 345	Gly	Ser	Gln	Glu	Phe 350	Ala	Arg
Leu	Leu	Ser 355	Thr	Ser	Tyr	Lys	Lys 360	Thr	His	Gly	Asn	Thr 365	Arg	Pro	Ser
Phe	Val 370	Tyr	Gly	Gln	Pro	Gly 375	Val	Ser	Gly	His	Tyr 380	Gly	Val	Gly	Pro
His 385	Asp	Lys	Thr	Ile	Ile 390	Glu	Asp	Ser	Ala	Gly 395	Ala	Ser	Gly	Leu	Ile 400
Arg	Asn	Asp	Asp	Asn 405	Met	Tyr	Glu	Asn	Ile 410	Gly	Ala	Phe	Asn	Asp 415	Val
His	Thr	Val	Asn 420	Gly	Ile	Lys	Arg	Gly 425	Ile	Tyr	Asp	Ser	11e 430	Lys	Tyr
Met	Leu	Phe 435	Thr	Asp	His	Leu	His 440	Gly	Asn	Thr	Tyr	Gly 445	His	Ala	Ile
Asn	Phe 450	Leu	Arg	Val	Asp	Lys 455	His	Asn	Pro	Asn	Ala 460	Pro	Val	Tyr	Leu
_	Phe	Ser	Thr	Ser		Val	Gly	Ser	Leu		Glu	His	Phe	Val	
465 Phe	Pro	Glu	Ser		470 Ile	Ala	Asn	His		475 Arg	Phe	Asn	Lys		480 Pro
Ile	Lys	Ala	Val	485 Gly	Ser	Thr	Lys	Asp	490 Tyr	Ala	Gln	Arg	Val	495 Gly	Thr

500 505 Val Ser Asp Thr Ile Ala Ala Ile Lys Gly Lys Val Ser Ser Leu Glu 520 525 Asn Arg Leu Ser Ala Ile His Gln Glu Ala Asp Ile Met Ala Ala Gln 535 540 Ala Lys Val Ser Gln Leu Gln Gly Lys Leu Ala Ser Thr Leu Lys Gln 550 555 560 Ser Asp Ser Leu Asn Leu Gln Val Arg Gln Leu Asn Asp Thr Lys Gly 570 575 565 Ser Leu Arg Thr Glu Leu Leu Ala Ala Lys Ala Lys Gln Ala Gln Leu 580 585 590 Glu Ala Thr Arg Asp Gln Ser Leu Ala Lys Leu Ala Ser Leu Lys Ala 600 Ala Leu His Gln Thr Glu Ala Leu Ala Glu Gln Ala Ala Ala Arg Val 615 Thr Ala Leu Val Ala Lys Lys Ala His Leu Gln Tyr Leu Arg Asp Phe 630 635 Lys Leu Asn Pro Asn Arg Leu Gln Val Ile Arg Glu Arg Ile Asp Asn 645 650 Thr Lys Gln Asp Leu Ala Lys Thr Thr Ser Ser Leu Leu Asn Ala Gln 665 670 Glu Ala Leu Ala Ala Leu Gln Ala Lys Gln Ser Ser Leu Glu Ala Thr 675 680 685 Ile Ala Thr Thr Glu His Gln Leu Thr Leu Lys Thr Leu Ala Asn 690 695 700 Glu Lys Glu Tyr Arg His Leu Asp Glu Asp Ile Ala Thr Val Pro Asp 710 715 Leu Gln Val Ala Pro Pro Leu Thr Gly Val Lys Pro Leu Ser Tyr Ser